

AMENDMENTS TO THE SPECIFICATION

Please amend the paragraph at page 27, lines 4-11 as follows:

Additional illustrative embodiments of the invention disclosed herein include 121P1F1 polypeptides comprising the amino acid residues of one or more of the biological motifs contained within a 121P1F1 polypeptide sequence set forth in Figure 2 or Figure 3. Various motifs are known in the art, and a protein can be evaluated for the presence of such motifs by a number of publicly available Internet sites (see, e.g., URL addresses: pfam.wustl.edu/; ~~http://searchlauncher.bcm.tmc.edu/seq-search/struc-predict.html~~; searchlauncher.bcm.tmc.edu/seq-search/struc-predict.html; psort.ims.u-tokyo.ac.jp/; www.cbs.dtu.dk/; www.ebi.ac.uk/interpro/scan.html; www.expasy.ch/tools/scnpsit1.html; Epimatrix™ and Epimer™, Brown University, www.brown.edu/Research/TB-HIV_Lab/epimatrix/epimatrix.html; and BIMAS, bimas.dcrf.nih.gov/).

Please amend the paragraph at page 76, lines 14-18 as follows:

A cDNA (clone A) of 863 bp was isolated from a Human Testis cDNA library, revealing an ORF of 205 amino acids (Figure 2 and Figure 3). It is probable that 121P1F1 is a cytoplasmic protein based on two topology algorithms (J. Mol. Biol. 2000, 300:1005 and Bioinformatics, 1998, 14:378) and based on its homology to Dynactin. However, it is also possible that 121P1F1 is localized in the nucleus based on PSORT analysis (~~http://psort.nibb.ac.jp:8800/form.html~~). (psort.nibb.ac.jp:8800/form.html).

Please amend the paragraph at page 76, lines 34-35 as follows:

121P1F1 maps to chromosome 4q, using 121P1F1 sequence and the NCBI BLAST tool:
 (<http://www.ncbi.nlm.nih.gov/genome/seq/page.cgi?F=HsBlast.html&&ORG=Hs>).
 (www.ncbi.nlm.nih.gov/genome/seq/page.cgi?F=HsBlast.html&&ORG=Hs).

Please replace the paragraphs (Table XXI) at page 196, line 1 to page 197, line 9 with the following paragraphs/table:

A. TABLE XXI: Properties of 121P1F1

121P1F1	Bioinformatic Program	URL	Outcome
ORF	ORF finder		618 bp
Protein length			205 aa
Transmembrane region	TM Pred	http://www.ch.embnet.org/	no TM
	HMMTop	http://www.enzim.hu/hmmtop/	no TM, intracellular
	Sosui	http://www.genome.ad.jp/SOSui/	no TM, soluble protein
	TMHMM	http://www.cbs.dtu.dk/services/TMHMM	no TM
Signal Peptide	Signal P	http://www.cbs.dtu.dk/services/SignalP/	none
pI	pI/MW tool	http://www.expasy.ch/tools/	8.28
Molecular weight	pI/MW tool	http://www.expasy.ch/tools/	23.7 kDa
Localization	PSORT	http://psort.nibb.ac.jp/	30% nuclear, 10% mitochondrial
	PSORT II	http://psort.nibb.ac.jp/	65% nuclear, 17% cytoplasmic
	Pfam	http://www.sanger.ac.uk/Pfam/	Basic Zipper motif, Myc leucine zipper
	Prints	http://www.biochem.ucl.ac.uk/	Steroid hormone receptor signature
	Blocks	http://www.blocks.fhcrc.org/	no significant motif
Variant 1A	Bioinformatic Program	URL	Outcome
ORF	ORF finder		618 bp
Protein length			126 aa
Transmembrane region	TM Pred	http://www.ch.embnet.org/	no TM
	HMMTop	http://www.enzim.hu/hmmtop/	no TM, extracellular
	Sosui	http://www.genome.ad.jp/SOSui/	no TM, soluble protein
	TMHMM	http://www.cbs.dtu.dk/services/TMHMM	no TM
Signal Peptide	Signal P	http://www.cbs.dtu.dk/services/SignalP/	none
pI	pI/MW tool	http://www.expasy.ch/tools/	8.65

Molecular weight	pI/MW tool	http://www.expasy.ch/tools/	14.3 kDa
Localization	PSORT	http://psort.nibb.ac.jp/	30% nuclear, 11% peroxisome
	PSORT II	http://psort.nibb.ac.jp/	30% nuclear, 52.2% cytoplasmic
Motifs	Pfam	http://www.sanger.ac.uk/Pfam/	no significant motif
	Prints	http://www.biochem.ucl.ac.uk/	no significant motif
	Blocks	http://www.blocks.fhcrc.org/	no significant motif

Variant 4	Bioinformatic Program	URL	Outcome
ORF	ORF finder		618 bp
Protein length			190 aa
Transmembrane region	TM Pred	http://www.ch.embnet.org/	no TM
	HMMTop	http://www.enzim.hu/hmmtop/	no TM, intracellular
	Sosui	http://www.genome.ad.jp/SOSui/	no TM, soluble protein
	TMHMM	http://www.cbs.dtu.dk/services/TMHMM	no TM
Signal Peptide	Signal P	http://www.cbs.dtu.dk/services/SignalP/	none
pI	pI/MW tool	http://www.expasy.ch/tools/	6.05
Molecular weight	pI/MW tool	http://www.expasy.ch/tools/	22.02 kDa
Localization	PSORT	http://psort.nibb.ac.jp/	30% nuclear, 10% mitochondrial matrix space, 10% lysosome
	PSORT II	http://psort.nibb.ac.jp/	65.2% nuclear, 21.7% mitochondrial, 13% cytoplasmic
Motifs	Pfam	http://www.sanger.ac.uk/Pfam/	bZip transcription factor
	Prints	http://www.biochem.ucl.ac.uk/	Myc leucine zipper
	Blocks	http://www.blocks.fhcrc.org/	steroid hormone receptor signature
			no significant motif